Amendments to the Claims:

1-8. (Canceled)

9. (Currently amended) A method for preparing a DNA fragment corresponding to a nucleotide sequence of ~~a~~ the most 5' end region of an mRNA, ~~wherein the region includes the most 5' end of the mRNA,~~ comprising the steps of:

(a) preparing a nucleic acid corresponding to a nucleotide sequence of the most 5' end of an mRNA, wherein preparing the nucleic acid comprises:

(i) synthesizing first-strand cDNAs using RNAs as a template and producing cDNA/RNA hybrids of the resulting first-strand cDNAs and the RNAs;

(ii) selecting a particular cDNA/RNA hybrid that has the 5' cap structure of the mRNA using a selective binding substance which specifically recognizes the 5' cap structure; and

(iii) recovering a nucleic acid corresponding to the most 5' end of the mRNA;

(b) attaching at least one linker to the end corresponding to the most 5' end of the mRNA in the nucleic acid;

(c) cleaving the nucleic acid with a restriction enzyme having its recognition site within the linker and its cleavage site within the nucleic acid corresponding to the most 5' end of the mRNA; and

(d) collecting a resulting DNA fragment corresponding to the most 5' end of the mRNA.

10. (Currently amended) The method according to claim 9, wherein the nucleic acid prepared in step (a) is a full-length cDNA, and wherein the selective binding substance is attached to a support.

11. (Canceled)

12. (Currently amended) A method for preparing a DNA fragment corresponding to a nucleotide sequence of a 5' end region of an mRNA, comprising the steps of~~, wherein the region includes the most 5' end of the mRNA~~:

(a) preparing a nucleic acid corresponding to a nucleotide sequence of the most 5' end of an mRNA, wherein preparing the nucleic acid comprises:

(i) synthesizing first strand cDNAs using RNAs as a template and producing cDNA/RNA hybrids of the resulting first strand cDNAs and the RNAs;

(ii) conjugating a selective binding substance to a 5' cap structure of an mRNA present in the RNAs;

(iii) contacting the cDNA/RNA hybrids with a support, wherein another matching selective binding substance is fixed to the support, and the matching selective binding substance specifically binds to the selective binding substance; and

(iv) recovering the ~~a~~ nucleic acid corresponding to the most 5' end of the mRNA from the mRNA fixed to the support;

(b) attaching at least one linker to the end corresponding to the most 5' end of the mRNA in the nucleic acid;

(c) cleaving the nucleic acid with a restriction enzyme having its recognition site within the linker and its cleavage site within the nucleic acid corresponding to the most 5' end of the mRNA; and

(d) collecting a resulting DNA fragment corresponding to the most 5' end of the mRNA.

13. (Previously Presented) The method according to claim 9, wherein the selective binding substance is a cap binding protein or a cap binding antibody.

14. (Original) The method according to claim 12, wherein the selective binding substance is biotin, and the matching selective binding substance is selected from the group consisting of avidin, streptavidin and a derivative therefrom which specifically binds to biotin.

15. (Original) The method according to claim 12, wherein the selective binding substance is digoxigenin and the matching selective binding substance is an antibody against digoxigenin.

16. (Previously Presented) The method according to claim 10, wherein the support is made of magnetic beads, agarose beads, latex beads, sepharose matrix, silicagel matrix or glass beads.

17. (Currently amended) A method for preparing a double-stranded DNA fragment comprising a nucleotide sequence of ~~a~~ the most 5' end region of an mRNA, ~~wherein the region includes the most 5' end of the mRNA,~~ comprising the steps of:

(a) preparing a nucleic acid corresponding to a nucleotide sequence of the most 5' end of an mRNA;

(b) attaching at least one linker to the nucleic acid, wherein attaching the linker comprises the steps of:

(i) attaching a linker to an end region corresponding to the nucleotide sequence of ~~a~~ the most 5' end region of the mRNA, wherein the linker carries at least one restriction enzyme recognition site for a restriction enzyme that cleaves a site different from its recognition sequence;

(ii) synthesizing a first strand cDNA ~~nucleic acid~~ using the mRNA having the linker as a template;

(iii) removing the mRNA; and

(iv) synthesizing a second strand cDNA using the first strand cDNA ~~nucleic acid~~ synthesized in step (iii) as a template;

(c) cleaving the nucleic acid with a restriction enzyme having its recognition site within the linker and its cleavage site within the nucleic acid corresponding to the most 5' end of the mRNA; and

(d) collecting a resulting double-stranded DNA fragment corresponding to the most 5' end of the mRNA.

18. (Canceled)

19. (Previously presented) The method according to claim 17, wherein the second-strand cDNA is synthesized using other oligonucleotides which are partially or totally complementary to the linker.

20. (Currently amended) The method according to claim 19, wherein a selective binding substance is attached to or included in the oligonucleotides, and ~~the~~ a collecting ~~recovering~~ step comprises the steps of binding the selective binding substance to a matching selective binding substance immobilized on a support, and recovering the support, wherein the matching selective binding substance specifically binds to the selective binding substance.

21. (Original) The method according to claim 20, wherein the selective binding substance is biotin, and the matching selective binding substance is selected from the group consisting of avidin, streptavidin and a derivative therefrom which specifically binds to biotin.

22. (Original) The method according to claim 20, wherein the selective binding substance is digoxigenin, and the matching selective binding substance is an antibody against digoxigenin.

23. (Currently amended) The method according to claim 17, wherein the restriction enzyme is ~~the~~ a Class II or Class III restriction enzyme.

24. (Currently amended) The method according to claim 17, wherein the restriction enzyme is selected from the group comprising the Class IIG and Class IIS restriction enzymes.

25. (Original) The method according to claim 23, wherein the restriction enzyme is selected from the group consisting of Gsu I, MmeI, BpmI, BsgI and EcoP15I.

26-33. (Canceled)

34. (Withdrawn) A concatemer prepared by the method according to claim 33.

35. (Withdrawn) A vector comprising the concatemer according to claim 34.

36. (Withdrawn) A sequence derived from the concatemer according to claim 34.

37. (Withdrawn) The method for determining the transcriptional states of a sample using a sequence derived from the DNA fragment prepared by the method according to claim 1.

38. (Withdrawn) The method for obtaining expression data on a plurality of mRNAs or cDNAs in a sample using a sequence derived from the DNA fragment prepared by the method according to claim 1.

39. (Withdrawn) The method quantifying expression data on a plurality of mRNAs in a sample using a sequence derived from the DNA fragment prepared by the method according to claim 1.

40. (Withdrawn) The method for building a database holding sequence information using a sequence derived from the DNA fragment prepared by the method according to claim 1.

41. (Withdrawn) The method identifying transcribed regions from a genomic sequence using a sequence derived from the DNA fragment prepared by the method according to claim 1.

42. (Withdrawn) The method for identifying a transcription initiation site and a related regulatory sequence in a genomic sequence using a sequence derived from the DNA fragment prepared by the method according to claim 1.

43. (Withdrawn) The method for cloning a full-length or partial cDNA from a cDNA library or biological sample using a sequence derived from the DNA fragment prepared by the method according to claim 1.

44. (Withdrawn) The method for cloning a complete or partial promoter region of a gene from a genomic library or genomic DNA using a sequence derived from the DNA fragment prepared by the method according to claim 1.

45. (Withdrawn) The method for analyzing the activity of regulatory regions in a genome based on genomic sequence information using a sequence derived from the DNA fragment prepared by the method according to claim 1.

46. (Withdrawn) The method for inactivating a gene or altering its expression using a sequence derived from the DNA fragment prepared by the method according to claim 1.

47. (Withdrawn) The method according to claim 46, wherein the gene is inactivated or altered in its expression by the means of siRNA or RNAi.

48. (Withdrawn) The method for synthesizing a nucleotide sequence to be used as the linker or primer based on a sequence derived from the DNA fragment prepared by the method according to claim 1.

49. (Withdrawn) The method for synthesizing a hybridization probe based on a sequence derived from the DNA fragment prepared by the method according to claim 1.

50. (Withdrawn) The method according to claim 49, wherein the hybridization probe is attached to a support.

51. (Withdrawn) The method according to claim 49, wherein the hybridization probe is a probe to identify the sequence corresponding to the nucleotide sequence of the 5' end region of the mRNA.

52-56. (Canceled)

57. (Previously Presented) The method according to claim 10, wherein the selective binding substance is a cap binding protein or a cap binding antibody.

58. (Previously Presented) The method according to claim 12, wherein the support is made of magnetic beads, agarose beads, latex beads, sepharose matrix, silicagel matrix or glass beads.